

SEQUENCE LISTING

<110> The University of Queensland (all designated States except US)
Frazer, Ian Hector and Zhou, Jian (US only)

<120> METHOD AND POLYNUCLEOTIDES FOR DETERMINING TRANSLATIONAL
EFFICIENCY OF A CODON

<130> 10338-5US

<140> Not yet assigned

<141> Herewith

<150> AU PP8078

<151> 1999-01-08

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<151> 2000-01-07

<160> 180

<170> PatentIn Ver. 2.0

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<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ala(GCA)5GFP

<220>

<221> CDS

<222> (1)..(732)

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20 25 30	

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ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
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65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	

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 210 215 220

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 Leu Tyr Lys

<210> 2
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 <213> Artificial Sequence

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 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
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09900345-070601

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
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 <222> (1)..(732)

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 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

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acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
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Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145				150					155					160	
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Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
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		195					200					205				
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ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
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 225 230 235 240

ctg tac aag tga 732
 Leu Tyr Lys

<210> 4
 <211> 243
 <212> PRT
 <213> Artificial Sequence

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 20 25 30
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 35 40 45
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile

	165		170		175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	180	185	190		
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	195	200	205		
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	210	215	220		
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Leu Tyr Lys					

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<220>
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<220>
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 <222> (1)..(732)

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Met Ala Ala Ala Ala Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
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gtc cca att ctg gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctg acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctg cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
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225 230 235 240	

732



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Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr
Leu	Lys 50	Phe	Ile	Cys	Thr	Thr 55	Gly	Lys	Leu	Pro	Val 60	Pro	Trp	Pro	Thr
Leu 65	Val	Thr	Thr	Phe	Ser 70	Tyr	Gly	Val	Gln	Cys 75	Phe	Ser	Arg	Tyr	Pro 80
Asp	His	Met	Lys	Gln 85	His	Asp	Phe	Phe	Lys 90	Ser	Ala	Met	Pro	Glu 95	Gly
Tyr	Val	Gln	Glu 100	Arg	Thr	Ile	Phe	Phe 105	Lys	Asp	Asp	Gly	Asn 110	Tyr	Lys
Thr	Arg	Ala 115	Glu	Val	Lys	Phe	Glu 120	Gly	Asp	Thr	Leu	Val 125	Asn	Arg	Ile
Glu	Leu 130	Lys	Gly	Ile	Asp	Phe 135	Lys	Glu	Asp	Gly	Asn 140	Ile	Leu	Gly	His
Lys 145	Leu	Glu	Tyr	Asn	Tyr 150	Asn	Ser	His	Asn	Val 155	Tyr	Ile	Met	Ala	Asp 160
Lys	Gln	Lys	Asn	Gly 165	Ile	Lys	Val	Asn	Phe 170	Lys	Ile	Arg	His	Asn 175	Ile
Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro

Figure 1 consists of 12 line drawings of a chick embryo at various stages of development, arranged vertically. The drawings are labeled with numbers 1 through 12. The stages are as follows:

- 1. Fertilized egg (single cell)
- 2. 2-cell stage
- 3. 4-cell stage
- 4. 8-cell stage
- 5. Morula stage (solid ball of cells)
- 6. Blastula stage (hollow ball of cells)
- 7. Gastrula stage (three germ layers visible)
- 8. Early neurulation stage (folded sheet of cells)
- 9. Late neurulation stage (folded sheet of cells)
- 10. Early hatching stage (beak and legs visible)
- 11. Late hatching stage (beak and legs visible)
- 12. Hatched chick (fully formed)

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
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 Leu Tyr Lys

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<220>
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 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

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Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

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Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
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	130					135					140					
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
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Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
	195						200					205				

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 9
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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
		100						105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230				235					240		
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 10

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 10
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu

225 230 235 240

Leu Tyr Lys

<210> 11
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Arg(AGG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 11
atg agg agg agg agg agg agc aag ggc gag gaa ctg ttc act ggc gtg 48
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	
<210> 12	
<211> 243	
<212> PRT	
<213> Artificial Sequence	
<400> 12	
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240
Leu Tyr Lys

<210> 13
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Arg(CGA)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 13
 atg cga cga cga cga cga agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

<400> 14
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 15
<211> 732
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Arg(CGC)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 15

atg	cg	cg	cg	cg	cg	ag	aa	gg	ga	ga	ct	tt	ac	gg	gt	48
Met	Arg	Arg	Arg	Arg	Arg	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5				10						15		
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
tct	gtc	agc	gga	gag	ggt	gaa	ggt	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55				60						
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70				75						80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85				90						95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cg	gct	gaa	gtc	aag	ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

ctg tac aag tga 732
Leu Tyr Lys

<210> 16
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 16
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr

09900345-00661

50		55		60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro				
65		70		75 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly				
	85		90	95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys				
	100		105	110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile				
	115		120	125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His				
	130		135	140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp				
	145		150	155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile				
	165		170	175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro				
	180		185	190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr				
	195		200	205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val				
	210		215	220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu				
	225		230	235 240
Leu Tyr Lys				

<210> 17
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Arg(CGG)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 17

atg	cgg	cgg	cgg	cgg	cgg	agc	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	48
Met	Arg	Arg	Arg	Arg	Arg	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5				10						15		
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65				70				75						80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85				90						95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130				135						140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

ctg tac aag tga 732
Leu Tyr Lys

<210> 18
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 18
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 19

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Arg(CGT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 19

atg	cgt	cgt	cgt	cgt	cgt	agc	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	48
Met	Arg	Arg	Arg	Arg	Arg	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5				10						15		
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65				70					75					80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145				150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

ctg tac aag tga 732
Leu Tyr Lys

<210> 20
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 20
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

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Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240
Leu Tyr Lys

<210> 21
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Asn(AAC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 21
atg aac aac aac aac aac agc aag ggc gag gaa ctg ttc act ggc gtg 48
Met Asn Asn Asn Asn Asn Ser Lys Gly Glu Glu Leu Phe Thr Gly Val

1				5				10				15				
gtc Val	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	ggg Gly	cac His 30	aaa Lys	ttt Phe	96
tct Ser	gtc Val	agc Ser 35	gga Gly	gag Glu	ggt Gly	gaa Glu	ggt Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	144
ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192
ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240
gac Asp	cat His	atg Met	aag Lys	cag Gln 85	cat His	gac Asp	ttt Phe	ttc Phe	aag Lys 90	agc Ser	gcc Ala	atg Met	ccc Pro	gag Glu 95	ggc Gly	288
tat Tyr	gtg Val	cag Gln 100	gag Glu	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	ggg Gly	aac Asn 110	tac Tyr	aag Lys	336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576

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<210> 22
<211> 243
<212> PRT
<213> Artificial Sequence
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115	120	125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His		
130	135	140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp		
145	150	155
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile		
	165	170
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro		
	180	185
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr		
	195	200
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val		
	210	215
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu		
225	230	235

Leu Tyr Lys

<210> 23
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Asn(AAT)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 23	
atg aat aat aat aat aat agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Asn Asn Asn Asn Asn Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	

-xxxiv-

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

ctg tac aag tga 732
Leu Tyr Lys

<210> 24
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 24
Met Asn Asn Asn Asn Asn Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140

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Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 25
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Asp(GAC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 25
atg gac gac gac gac gac agc aag ggc gag gaa ctg ttc act ggc gtg 48
Met Asp Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr

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-xxxvii-

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

ctg tac aag tga 732
 Leu Tyr Lys

<210> 26
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<400> 26
 Met Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

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Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240
Leu Tyr Lys

<210> 27
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Asp(GAT)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 27
atg gat gat gat gat gat agc aag ggc gag gaa ctg ttc act ggc gtg 48
Met Asp Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
gtc cca att ctg gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctg acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
ctg aaa ttc atc tgc acc act gga aag ctg cct gtg cca tgg cca aca 192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr

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50					55					60						
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230					235					240	

ctg tac aag tga
Leu Tyr Lys

732

<210> 28
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 28

Met	Asp	Asp	Asp	Asp	Asp	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	1	5	10	15
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	20	25	30	
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	35	40	45	
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	50	55	60	
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	65	70	75	80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	85	90	95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	100	105	110	
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	115	120	125	
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	130	135	140	
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	145	150	155	160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	165	170	175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro				

180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 Leu Tyr Lys

<210> 29
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Cys(TGC)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 29
 atg tgc tgc tgc tgc tgc agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Cys Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro

65		70		75		80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288						
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly							
		85		90		95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336						
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys		100		105		110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384						
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile		115		120		125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432						
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His		130		135		140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480						
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp		145		150		155	160
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528						
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile		165		170		175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576						
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro		180		185		190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624						
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr		195		200		205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672						
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val		210		215		220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720						
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu		225		230		235	240
ctg tac aag tga	732						
Leu Tyr Lys							

<210> 30
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<400> 30

Met Cys Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 31
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cys(TGT)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 31
atg tgt tgt tgt tgt tgt agc aag ggc gag gaa ctg ttc act ggc gtg 48
Met Cys Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
gtc cca att ctg gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctg acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
ctg aaa ttc atc tgc acc act gga aag ctg cct gtg cca tgg cca aca 192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly

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85										90					95					
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336				
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys					
		100						105					110							
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aac	aga	atc	384				
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile					
		115					120					125								
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432				
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His					
	130					135					140									
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aac	gtg	tac	atc	atg	gcc	gac	480				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp					
145					150					155					160					
aag	caa	aag	aac	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528				
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile					
			165						170					175						
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576				
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro					
			180					185					190							
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624				
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr					
		195					200					205								
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672				
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val					
	210					215					220									
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720				
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu					
225					230					235					240					
ctg	tac	aag	tga													732				
Leu	Tyr	Lys																		

<210> 32
 <211> 243
 <212> PRT

<213> Artificial Sequence

<400> 32

Met	Cys	Cys	Cys	Cys	Cys	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	1		5		10		15
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	20		25		30		
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	35		40		45		
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	50		55		60		
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	65		70		75		80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	85		90		95		
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	100		105		110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	115		120		125		
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	130		135		140		
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	145		150		155		160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	165		170		175		
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	180		185		190		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	195		200		205		
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	210		215		220		

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 33
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gln(CAA)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 33
atg caa caa caa caa caa agc aag ggc gag gaa ctg ttc act ggc gtg 48
Met Gln Gln Gln Gln Gln Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys

100										105										110										
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	384														
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile															
115						120			125																					
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432														
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His															
130						135			140																					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480														
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp															
145			150			155			160																					
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528														
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile															
			165			170			175																					
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576														
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro															
			180			185			190																					
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624														
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr															
			195			200			205																					
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672														
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val															
210			215			220																								
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720														
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu															
225			230			235			240																					
ctg	tac	aag	tga												732															
Leu	Tyr	Lys																												

<210> 34
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<400> 34
 Met Gln Gln Gln Gln Gln Ser Lys Gly Glu Glu Leu Phe Thr Gly Val

1	5	10	15
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	20	25	30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	35	40	45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	50	55	60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	65	70	75
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	85	90	95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	100	105	110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	115	120	125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	130	135	140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	145	150	155
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	165	170	175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	180	185	190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	195	200	205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	210	215	220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	225	230	235
Leu Tyr Lys			240

<210> 35
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Gln(CAG)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 35
 atg cag cag cag cag cag agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Gln Gln Gln Gln Gln Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile

115	120	125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140			432
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160			480
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175			528
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190			576
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205			624
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220			672
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240			720
ctg tac aag tga Leu Tyr Lys			732
<210> 36			
<211> 243			
<212> PRT			
<213> Artificial Sequence			
<400> 36			
Met Gln Gln Gln Gln Gln Ser Lys Gly Glu Glu Leu Phe Thr Gly Val 1 5 10 15			
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30			

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240
Leu Tyr Lys

<210> 37
<211> 732

<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Glu(GAA)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 37

atg gaa gaa gaa gaa gaa agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Glu Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	

130	135	140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac			480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp			
145	150	155	160
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att			528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile			
	165	170	175
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca			576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro			
	180	185	190
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc			624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
	195	200	205
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc			672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
	210	215	220
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag			720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
	225	230	235
ctg tac aag tga			732
Leu Tyr Lys			
<p><210> 38</p> <p><211> 243</p> <p><212> PRT</p> <p><213> Artificial Sequence</p>			
<p><400> 38</p> <p>Met Glu Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val</p> <p>1 5 10 15</p> <p>Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe</p> <p>20 25 30</p> <p>Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr</p> <p>35 40 45</p>			

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 Leu Tyr Lys

<210> 39
 <211> 732
 <212> DNA
 <213> Artificial Sequence
 <220>

<223> Description of Artificial Sequence: Glu(GAG)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 39

atg	gag	gag	gag	gag	gag	agc	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	48
Met	Glu	Glu	Glu	Glu	Glu	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5				10						15		
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
tct	gtc	agc	gga	gag	ggt	gaa	ggt	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55				60						
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70				75						80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85				90						95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130				135						140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	

145	150	155	160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att				528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile				
	165	170	175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca				576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro				
	180	185	190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc				624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr				
	195	200	205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc				672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val				
	210	215	220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag				720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu				
	225	230	235	240
ctg tac aag tga				732
Leu Tyr Lys				
<210> 40				
<211> 243				
<212> PRT				
<213> Artificial Sequence				
<400> 40				
Met Glu Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val				
1 5 10 15				
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe				
20 25 30				
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr				
35 40 45				
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr				
50 55 60				
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro				

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65		70		75		80									
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
				85					90					95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
		100						105					110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	130					135					140				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
145					150					155					160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
			165						170					175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
			180					185					190		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
		195					200					205			
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val
	210					215					220				
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu
225					230					235					240
Leu	Tyr	Lys													

<210> 41
 <211> 732
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Gly(GGA)5GFP
 <220>
 <221> CDS

165										170					175					
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576				
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro					
			180					185					190							
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624				
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr					
		195					200					205								
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672				
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val					
	210					215					220									
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720				
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu					
225					230				235						240					
ctg	tac	aag	tga													732				
Leu	Tyr	Lys																		
<210> 42																				
<211> 243																				
<212> PRT																				
<213> Artificial Sequence																				
<400> 42																				
Met	Gly	Gly	Gly	Gly	Gly	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val					
1				5					10					15						
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe					
			20					25					30							
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr					
		35					40					45								
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr					
	50					55					60									
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro					
65					70					75					80					
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly					
				85					90					95						

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 43
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gly(GGC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 43
atg ggc ggc ggc ggc ggc agc aag ggc gag gaa ctg ttc act ggc gtg 48

Met	Gly	Gly	Gly	Gly	Gly	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val		
1				5					10					15			
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe		
			20					25					30				
tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144	
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr		
		35					40					45					
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192	
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr		
	50					55					60						
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240	
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro		
	65				70				75						80		
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly		
				85					90					95			
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys		
			100					105					110				
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384	
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile		
		115					120					125					
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432	
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His		
	130				135						140						
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480	
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp		
	145				150					155					160		
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile		
				165					170					175			
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro		

180										185										190										
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624														
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr															
		195					200					205																		
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672														
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val															
	210					215					220																			
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720														
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu															
	225				230					235					240															
ctg	tac	aag	tga													732														
Leu	Tyr	Lys																												

<210> 44
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<400> 44
 Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 45
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gly(GGG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 45
atg ggg ggg ggg ggg ggg agc aag ggc gag gaa ctg ttc act ggc gtg 48
Met Gly Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96

Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70				75						80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	

05900345-070604

195	200	205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc			672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
210	215	220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag			720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
225	230	235	240
ctg tac aag tga			732
Leu Tyr Lys			

<210> 46
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<400> 46
 Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His

130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

Leu Tyr Lys

<210> 47
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Gly(GGT)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 47

atg ggt ggt ggt ggt ggt agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144

Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggc	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130				135						140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	

210	215	220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag			720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
225	230	235	240

ctg tac aag tga	732
Leu Tyr Lys	

<210> 48
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<400> 48

Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240
Leu Tyr Lys

<210> 49
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: His(CAC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 49
atg cac cac cac cac cac agc aag ggc gag gaa ctg ttc act ggc gtg 48
Met His His His His His Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192

Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50						55				60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65				70				75						80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aac	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aac	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145				150				155						160	
aag	caa	aag	aac	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	

240

732

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<210> 50
<211> 243
<212> PRT
<213> Artificial Sequence
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<400> 50

Met His His His His His Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 Leu Tyr Lys

<210> 51
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: His(CAT)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 51
 atg cat cat cat cat cat agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met His His His His His Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240

Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130				135						140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145				150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 52
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<400> 52

Met	His	His	His	His	His	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val
1				5					10					15	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe
			20					25					30		
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
	65				70					75					80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
				85					90					95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
			100					105					110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	130					135					140				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
145					150					155					160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
				165					170					175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
			180					185					190		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr

195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 53
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ile(ATA)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 53

atg	ata	ata	ata	ata	ata	agc	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	48
Met	Ile	Ile	Ile	Ile	Ile	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5					10					15		
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
tct	gtc	agc	gga	gag	ggt	gaa	ggt	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70				75						80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288

Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly		
				85					90					95			
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys		
			100					105					110				
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aac	aga	atc	384	
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile		
		115					120					125					
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432	
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His		
	130					135					140						
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aac	gtg	tac	atc	atg	gcc	gac	480	
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp		
145					150					155					160		
aag	caa	aag	aac	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile		
			165						170					175			
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro		
			180					185					190				
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624	
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr		
		195					200					205					
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672	
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val		
	210					215					220						
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720	
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu		
225					230					235					240		
ctg	tac	aag	tga													732	
Leu	Tyr	Lys															

<210> 54
<211> 243

<212> PRT

<213> Artificial Sequence

<400> 54

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Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1           5           10           15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
          20           25           30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
          35           40           45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
  50           55           60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
  65           70           75           80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
          85           90           95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
          100          105          110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
          115          120          125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
          130          135          140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
          145          150          155          160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
          165          170          175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
          180          185          190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
          195          200          205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
          210          215          220

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Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 55
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ile(ATC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 55
atg atc atc atc atc atc agc aag ggc gag gaa ctg ttc act ggc gtg 48
Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
gtc cca att ctg gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctg acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
ctg aaa ttc atc tgc acc act gga aag ctg cct gtg cca tgg cca aca 192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336

Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggc	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
		130				135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
		145			150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
		210				215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
		225			230				235						240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 56

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 56

-lxxxii-

Leu Tyr Lys

<210> 57
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ile(ATT)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 57
 atg att att att att att agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384

Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile		
		115					120					125					
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432	
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His		
		130				135					140						
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480	
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp		
		145			150					155					160		
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile		
				165					170					175			
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro		
			180					185					190				
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624	
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr		
		195					200					205					
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672	
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val		
		210				215					220						
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720	
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu		
		225			230				235						240		
ctg	tac	aag	tga													732	
Leu	Tyr	Lys															
<p><210> 58</p> <p><211> 243</p> <p><212> PRT</p> <p><213> Artificial Sequence</p> <p><400> 58</p> <p>Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val</p> <p>1 5 10 15</p> <p>Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe</p>																	

20										25										30										
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr															
		35					40					45																		
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr															
	50					55					60																			
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro															
	65				70					75					80															
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly															
				85					90					95																
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys															
		100					105						110																	
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile															
		115					120					125																		
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His															
	130					135					140																			
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp															
	145				150					155					160															
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile															
				165					170					175																
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro															
			180					185					190																	
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr															
		195					200					205																		
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val															
	210					215					220																			
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu															
	225				230					235					240															
Leu	Tyr	Lys																												

<210> 59

<211> 732
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu(CTA)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 59

atg cta cta cta cta cta agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432

Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His		
130						135					140						
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480	
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	160	
145				150						155							
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	175	
				165					170								
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	190	
			180					185									
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624	
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	205	
		195					200					205					
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672	
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	220	
	210					215											
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720	
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	240	
225					230					235							
ctg	tac	aag	tga													732	
Leu	Tyr	Lys															
<210>	60																
<211>	243																
<212>	PRT																
<213>	Artificial Sequence																
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Met	Leu	Leu	Leu	Leu	Leu	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val		
1					5				10					15			
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe		
			20					25					30				
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr		
		35					40					45					

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 61
<211> 732
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu(CTC)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 61

atg ctc ctc ctc ctc ctc agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480

Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														
<210> 62																
<211> 243																
<212> PRT																
<213> Artificial Sequence																
<400> 62																
Met	Leu	Leu	Leu	Leu	Leu	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5					10					15		
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240
Leu Tyr Lys

<210> 63

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu(CTG)5GFP

<220>

09900345.070601

-xcii-

Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230				235						240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														
<210> 64																
<211> 243																
<212> PRT																
<213> Artificial Sequence																
<400> 64																
Met	Leu	Leu	Leu	Leu	Leu	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5					10					15		
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	

				85					90					95			
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys		
			100					105					110				
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile		
		115					120					125					
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His		
	130					135					140						
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp		
145					150					155					160		
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile		
			165						170					175			
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro		
			180					185					190				
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr		
		195					200					205					
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val		
	210					215					220						
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu		
225					230					235					240		
Leu	Tyr	Lys															

<210> 65
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Leu(CTT)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 65

atg	ctt	ctt	ctt	ctt	ctt	agc	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	48
Met	Leu	Leu	Leu	Leu	Leu	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5					10					15		
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70				75						80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130				135						140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576

1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2

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<400> 66
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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
          35           40           45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50           55           60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
    65           70           75           80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
          85           90           95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
          100           105           110

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Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 67

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu(TTA)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 67

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1 5 10 15

-xcviii-

Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr		
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cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672	
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val		
	210					215					220						
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720	
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu		
225					230					235					240		
ctg	tac	aag	tga													732	
Leu	Tyr	Lys															

<210> 68
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<400> 68
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 20 25 30
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 Leu Tyr Lys

<210> 69
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Leu(TTG)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 69
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 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

-ci-

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

ctg tac aag tga 732
 Leu Tyr Lys

<210> 70
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<400> 70
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 1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp

145		150		155		160									
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
			165						170					175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
			180					185					190		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
		195					200					205			
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val
	210					215					220				
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu
225					230					235					240
Leu	Tyr	Lys													

<210> 71
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Lys(AAA)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	

-civ-

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

ctg tac aag tga
Leu Tyr Lys

732

<210> 72
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 72
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1 5 10 15
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240
Leu Tyr Lys

<210> 73
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Lys(AAG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 73
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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

Leu Tyr Lys

<210> 74

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 74

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		20						25					30		
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65					70					75					80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
				85					90					95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
		100						105					110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	130					135					140				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
145					150					155					160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
			165						170				175		
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
			180					185					190		

<400>																75	
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Met	Phe	Phe	Phe	Phe	Phe	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val		
1					5				10					15			
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gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe		
			20					25					30				
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tct	gtc	agc	gga	gag	ggt	gaa	ggt	gat	gcc	aca	tac	gga	aag	ctc	acc	144	
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr		
		35					40					45					
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ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192	
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr		
	50					55					60						
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Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro		
65					70					75					80		

<211> 243
<212> PRT
<213> Artificial Sequence

<400> 76

Met	Phe	Phe	Phe	Phe	Phe	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	1	5	10	15
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Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	35	40	45	
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	50	55	60	
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	65	70	75	80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	85	90	95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	100	105	110	
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	115	120	125	
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	130	135	140	
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	145	150	155	160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	165	170	175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	180	185	190	
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	195	200	205	
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val				

210	215	220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu		
225	230	235 240

Leu Tyr Lys

<210> 77
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Phe(TTC)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 77	
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1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	

tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
		100						105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195				200						205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230				235						240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 78
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<400> 78

Met	Phe	Phe	Phe	Phe	Phe	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val
1				5					10					15	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe
			20					25					30		
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65					70					75					80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
				85					90					95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
			100					105					110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	130					135					140				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
145					150					155					160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
				165					170					175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
			180					185					190		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
	195					200						205			
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val
	210					215					220				
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu
225					230					235					240

109000340050

Leu Tyr Lys

<210> 79
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Pro(CCC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 79
atg ccc ccc ccc ccc ccc agc aag ggc gag gaa ctg ttc act ggc gtg 48
Met Pro Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	
<210> 80	
<211> 243	
<212> PRT	
<213> Artificial Sequence	
<400> 80	
Met Pro Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	

<210> 81
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Pro(CCG)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 81
 atg ccg ccg ccg ccg ccg agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Pro Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

ctg tac aag tga 732
Leu Tyr Lys

<210> 82

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 82

Met Pro Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr

35	40	45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr		
50	55	60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro		
65	70	75
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly		
	85	90
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys		
	100	105
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile		
	115	120
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His		
	130	135
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp		
	145	150
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile		
	165	170
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro		
	180	185
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr		
	195	200
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val		
	210	215
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu		
	225	230
		235
Leu Tyr Lys		

<210> 83
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Pro(CCT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 83

atg cct cct cct cct cct agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Pro Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	

Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65					70					75					80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
				85					90					95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
		100					105						110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	130					135					140				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
145					150					155					160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
				165					170					175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
			180					185					190		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
		195					200					205			
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val
	210					215					220				
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu
225					230					235					240
Leu	Tyr	Lys													

<210> 85
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Pro(CGA)5GFP

<400> 85

-CXXIV-

Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200						205			
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230					235					240	
Leu	Tyr	Lys														

<210> 87
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ser(AGC)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 87

atg agc agc agc agc agc agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctg gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctg acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctg cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctg ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 88
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<400> 88
 Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys

100					105					110					
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	130					135					140				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
	145					150					155				160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
				165					170					175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
			180					185					190		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
		195					200					205			
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val
	210					215					220				
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu
	225					230					235				240
Leu	Tyr	Lys													

<210> 89
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ser(AGT)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 89
 atg agt agt agt agt agt agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Ser Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

Leu Tyr Lys

<210> 91
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ser(TCA)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 91
 atg tca tca tca tca tca agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Ser Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 93

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ser(TCC)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 93

atg tcc tcc tcc tcc tcc agc aag ggc gag gaa ctg ttc act ggc gtg 48
Met Ser Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

-CXXXVI-


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<210> 95
<211> 732
<212> DNA
<213> Artificial Sequence
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<220>  
<221> CDS  
<222> (1)..(732)
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-CXXXVIII-

ctg tac aag tga
Leu Tyr Lys

732

<210> 96
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 96

Met	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val
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Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 Leu Tyr Lys

<210> 97
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ser(TCT)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 97
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 Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 98
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<400> 98

Met	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val
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Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65				70					75					80	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145				150					155					160	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195				200						205				

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 99
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Thr(ACA)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 99
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Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
		100						105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230				235					240		
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 100

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 100

Met	Thr	Thr	Thr	Thr	Thr	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val
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Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe
			20					25					30		
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65					70					75					80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
				85					90					95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
			100					105					110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	130					135					140				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
145					150					155					160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
				165					170					175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
			180					185					190		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
	195					200						205			
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val
	210					215					220				
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu

225 230 235 240

Leu Tyr Lys

<210> 101
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Thr(ACC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 101
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Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 102
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<400> 102
 Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240
Leu Tyr Lys

<210> 103
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Thr(ACG)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

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 1 5 10 15
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 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctg acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 ctg aaa ttc atc tgc acc act gga aag ctg cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

ctg tac aag tga 732
Leu Tyr Lys

<210> 104
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 104
Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240
Leu Tyr Lys

<210> 105
<211> 732
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Thr(ACT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 105

atg act act act act act agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	

50					55					60					
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65					70					75					80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
				85					90					95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
			100					105					110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	130					135					140				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
145					150					155					160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
				165					170					175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
			180					185					190		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
		195				200						205			
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val
	210					215					220				
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu
225					230					235					240
Leu	Tyr	Lys													

<210> 107

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trp(TGG)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 107

atg	tgg	tgg	tgg	tgg	tgg	agc	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	48
Met	Trp	Trp	Trp	Trp	Trp	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5				10						15		
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65				70				75						80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85				90						95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130				135						140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

ctg tac aag tga 732
Leu Tyr Lys

<210> 108
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 108
Met Trp Trp Trp Trp Trp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
				85					90					95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
			100					105					110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	130					135					140				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
145					150					155					160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
			165						170					175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
			180					185					190		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
		195					200					205			
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val
	210					215					220				
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu
225					230					235					240
Leu	Tyr	Lys													

<210> 109

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Tyr(TAT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 109

atg	tat	tat	tat	tat	tat	agc	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	48
Met	Tyr	Tyr	Tyr	Tyr	Tyr	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5				10						15		
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155				160		
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

ctg tac aag tga 732
Leu Tyr Lys

<210> 110
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 110
Met Tyr Tyr Tyr Tyr Tyr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 111
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Tyr(TAC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 111
atg tac tac tac tac tac agc aag ggc gag gaa ctg ttc act ggc gtg 48
Met Tyr Tyr Tyr Tyr Tyr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val

1			5			10			15								
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe		
			20				25			30							
tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144	
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr		
			35				40			45							
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192	
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr		
			50				55			60							
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240	
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro		
			65	70			75			80							
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly		
			85			90			95								
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys		
			100			105			110								
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384	
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile		
			115			120			125								
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432	
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His		
			130			135			140								
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480	
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp		
			145			150			155			160					
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile		
			165			170			175								
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro		
			180			185			190								

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<400> 112
Met Tyr Tyr Tyr Tyr Tyr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1          5          10          15
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
          20          25          30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
          35          40          45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
          50          55          60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
          65          70          75          80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
          85          90          95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
          100          105          110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile

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115	120	125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His		
130	135	140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp		
145	150	155
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile		
	165	170
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro		
	180	185
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr		
	195	200
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val		
	210	215
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu		
	225	230
		235
Leu Tyr Lys		

<210> 113
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Val(GTA)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 113	
atg gta gta gta gta gta agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	

-clxv-

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

ctg tac aag tga 732
Leu Tyr Lys

<210> 114
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 114
Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 115
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Val(GTC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 115
atg gtc gtc gtc gtc gtc agc aag ggc gag gaa ctg ttc act ggc gtg 48
Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr

35	40	45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60			192
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80			240
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95			288
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110			336
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125			384
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140			432
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160			480
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175			528
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190			576
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205			624
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220			672

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

ctg tac aag tga 732
 Leu Tyr Lys

<210> 116
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<400> 116
 Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

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<210> 117
<211> 732
<212> DNA
<213> Artificial Sequence
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<220>  
<221> CDS  
<222> (1)..(732)
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50	55	60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80			240
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95			288
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110			336
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125			384
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140			432
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160			480
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175			528
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190			576
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205			624
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220			672
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240			720

ctg tac aag tga
Leu Tyr Lys

732

<210> 118
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 118
Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro

	180		185		190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	195		200		205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	210		215		220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	225		230		235
					240
Leu Tyr Lys					

<210> 119
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Val(GTT)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 119	
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Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	

65	70	75	80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	85	90	95	288
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	100	105	110	336
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	115	120	125	384
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	130	135	140	432
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	145	150	155	480
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	165	170	175	528
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	180	185	190	576
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	195	200	205	624
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	210	215	220	672
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	225	230	235	720
ctg tac aag tga Leu Tyr Lys				732

<210> 120
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<400> 120

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Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1              5              10              15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
      20              25              30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
      35              40              45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
      50              55              60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
      65              70              75              80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
      85              90              95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
      100              105              110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
      115              120              125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
      130              135              140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
      145              150              155              160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
      165              170              175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
      180              185              190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
      195              200              205
    
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Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 121

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Stop(TAA)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 121

atg	taa	taa	taa	taa	taa	agc	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	48
Met						Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5					10					15		

gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			

tct	gtc	agc	gga	gag	ggt	gaa	ggt	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				

ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					

ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	

gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly		
				85					90					95			
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys		
			100					105					110				
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aac	aga	atc	384	
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile		
		115					120					125					
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432	
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His		
	130					135					140						
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aac	gtg	tac	atc	atg	gcc	gac	480	
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp		
145					150					155					160		
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile		
				165					170					175			
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro		
			180					185					190				
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624	
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr		
		195					200					205					
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672	
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val		
	210					215					220						
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720	
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu		
225					230					235					240		
ctg	tac	aag	tga													732	
Leu	Tyr	Lys															

<210> 122

<211> 732

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Stop(TAG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 122
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Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432

Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
130						135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145				150						155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 123

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Stop(TGA)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 123

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Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576

Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 124
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<220>
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<220>
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<400>	124															
atg	agc	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	gtc	cca	att	ctc	gtg	48
Met	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
1				5					10					15		
gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	tct	gtc	agc	gga	gag	96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
			20					25					30			
ggt	gaa	ggt	gat	gcc	aca	tac	gga	aag	ctc	acc	ctg	aaa	ttc	atc	tgc	144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
		35					40					45				

acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	ctg	gtc	act	acc	ttc	192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	
	50					55					60					
tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	gac	cat	atg	aag	cag	240
Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	
65					70					75					80	
cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	tat	gtg	cag	gag	aga	288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
				85					90					95		
acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	acc	cgc	gct	gaa	gtc	336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
			100					105					110			
aag	ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	gag	ctg	aag	ggc	att	384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
		115					120					125				
gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	aag	ctg	gaa	tac	aac	432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
	130					135					140					
tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	aag	caa	aag	aat	ggc	480
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	
145					150				155						160	
atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	gag	gat	gga	tcc	gtg	528
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	
				165					170					175		
cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	atc	ggc	gac	ggc	cct	576
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	
			180					185					190			
gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	cag	tct	gcc	ctg	tct	624
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	
		195					200					205				
aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	ctg	ctg	gag	ttt	gtg	672
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	
	210					215					220					
acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	ctg	tac	aag	tga		717

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 125
<211> 238
<212> PRT
<213> Artificial Sequence

<400> 125
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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 126
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ala(GCA)5
primer

<400> 126
cggggtacca tggcagcagc agcagcaagc aagggcgagg aactgttcac tggc 54

<210> 127
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ala(GCC)5
primer

<400> 127
cggggtacca tggccgccgc cgccgcccgc aagggcgagg aactgttcac tggc 54

<210> 128
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ala(GCG)5
primer

<400> 128
cggggtacca tggcggcggc ggcggcgagc aagggcgagg aactgttcac tggc 54

<210> 1293
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ala(GCT)5
primer

<400> 129
cggggtacca tggctgctgc tgctgctagc aagggcgagg aactgttcac tggc 54

<210> 130
<211> 54
<212> DNA
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<220>
<223> Description of Artificial Sequence: Arg(AGA)5
primer

<400> 130
cggggtacca tgagaagaag aagaagaagc aagggcgagg aactgttcac tggc 54

<210> 131
<211> 54
<212> DNA
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<220>
<223> Description of Artificial Sequence: Arg(AGG)5
primer

<400> 131
cggggtacca tgaggaggag gaggaggagc aagggcgagg aactgttcac tggc 54

<210> 132

<211> 54
<212> DNA
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<220>

<223> Description of Artificial Sequence: Arg(CGA)5
primer

<400> 132
cggggtacca tgcgacgacg acgacgaagc aagggcgagg aactgttcac tggc 54

<210> 133
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<220>

<223> Description of Artificial Sequence: Arg(CGC)5
primer

<400> 133
cggggtacca tgcgccgccg ccgccgcagc aagggcgagg aactgttcac tggc 54

<210> 134
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<212> DNA
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<220>

<223> Description of Artificial Sequence: Arg(CGG)5
primer

<400> 134
cggggtacca tgcggcgggc gcggcggagc aagggcgagg aactgttcac tggc 54

<210> 135
<211> 54
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<220>

<223> Description of Artificial Sequence: arg(CGT)5

primer

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<210> 136
<211> 54
<212> DNA
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<220>
<223> Description of Artificial Sequence: Asn(AAC)5
primer

<400> 136
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<210> 137
<211> 54
<212> DNA
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<220>
<223> Description of Artificial Sequence: Asn(AAT)5
primer

<400> 137
cggggtacca tgaataataa taataatagc aagggcgagg aactgttcac tggc 54

<210> 138
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<220>
<223> Description of Artificial Sequence: Asp(GAC)5
primer

<400> 138
cggggtacca tggacgacga cgacgacagc aagggcgagg aactgttcac tggc 54

<210> 139
<211> 54
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<220>

<223> Description of Artificial Sequence: Asp(GAT)5
primer

<400> 139
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<210> 140
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<220>

<223> Description of Artificial Sequence: Cys(TGC)5
primer

<400> 140
cggggtacca tgtgctgctg ctgctgcagc aagggcgagg aactgttcac tggc 54

<210> 141
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<212> DNA
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<220>

<223> Description of Artificial Sequence: Cys(TGT)5
primer

<400> 141
cggggtacca tgtgttggtg ttgttgtagc aagggcgagg aactgttcac tggc 54

<210> 142
<211> 54
<212> DNA
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<220>

<223> Description of Artificial Sequence: Gln(CAA)5
primer

<400> 142
cggggtacca tgcaacaaca acaacaaagc aagggcgagg aactgttcac tggc 54

<210> 143
<211> 54
<212> DNA
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<220>
<223> Description of Artificial Sequence: Gln(CAG)5
primer

<400> 143
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<210> 144
<211> 54
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<220>
<223> Description of Artificial Sequence: Glu(GAA)5
primer

<400> 144
cggggtacca tggaagaaga agaagaaagc aagggcgagg aactgttcac tggc 54

<210> 145
<211> 54
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<220>
<223> Description of Artificial Sequence: Glu(GAG)5
primer

<400> 145
cggggtacca tggaggagga ggaggagagc aagggcgagg aactgttcac tggc 54

<210> 146
<211> 54
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<220>
<223> Description of Artificial Sequence: Gly(GGA)5
primer

<400> 146
cggggtacca tgggaggagg aggaggaaagc aagggcgagg aactgttcac tggc 54

<210> 147
<211> 54
<212> DNA
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<220>
<223> Description of Artificial Sequence: Gly(GGC)5
primer

<400> 147
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<210> 148
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gly(GGG)5
primer

<400> 148
cggggtacca tggggggggg gggggggagc aagggcgagg aactgttcac tggc 54

<210> 149
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Gly(GGT)5
primer

<400> 149
cgggggtacca tgggtggtgg tgggtggtagc aagggcgagg aactgttcac tggc 54

<210> 150
<211> 54
<212> DNA
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<220>
<223> Description of Artificial Sequence: His(CAC)5
primer

<400> 150
cgggggtacca tgcaccacca ccaccacagc aagggcgagg aactgttcac tggc 54

<210> 151
<211> 54
<212> DNA
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<220>
<223> Description of Artificial Sequence: His(CAT)5
primer

<400> 151
cgggggtacca tgcacatca tcatcatagc aagggcgagg aactgttcac tggc 54

<210> 152
<211> 54
<212> DNA
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<220>
<223> Description of Artificial Sequence: Ile(ATA)5
primer

<400> 152
cgggggtacca tgataataat aataataagc aagggcgagg aactgttcac tggc 54

<210> 153
<211> 54
<212> DNA
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<220>
<223> Description of Artificial Sequence: Ile(ATC)5
primer

<400> 153
cggggtacca tgatcatcat catcatcagc aagggcgagg aactgttcac tggc 54

<210> 154
<211> 54
<212> DNA
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<220>
<223> Description of Artificial Sequence: Ile(ATT)5
primer

<400> 154
cggggtacca tgattattat tattattagc aagggcgagg aactgttcac tggc 54

<210> 155
<211> 54
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<220>
<223> Description of Artificial Sequence: Leu(CTA)5
primer

<400> 155
cggggtacca tgctactact actactaagc aagggcgagg aactgttcac tggc 54

<210> 156
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<220>

<223> Description of Artificial Sequence: Leu(CTC)5
primer

<400> 156

cggggtacca tgctcctcct cctcctcagc aagggcgagg aactgttcac tggc 54

<210> 157

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu(CTG)5
primer

<400> 157

cggggtacca tgctgctgct gctgctgagc aagggcgagg aactgttcac tggc 54

<210> 158

<211> 54

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Leu(CTT)5
primer

<400> 158

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<210> 159

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu(TTA)5
primer

<400> 159

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<210> 160
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(TTG)5
primer

<400> 160
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<210> 161
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Lys(AAA)5
primer

<400> 161
cggggtacca tgaaaaaaaa aaaaaaaagc aagggcgagg aactgttcac tggc 54

<210> 162
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Lys(AAG)5
primer

<400> 162
cggggtacca tgaagaagaa gaagaagagc aagggcgagg aactgttcac tggc 54

<210> 163
<211> 54
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Phe(CTT)5
primer

<400> 163

cggggtacca tgcttcttct tcttcttagc aagggcgagg aactgttcac tggc 54

<210> 164

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Phe(TTC)5
primer

<400> 164

cggggtacca tggtcttctt cttcttcagc aagggcgagg aactgttcac tggc 54

<210> 165

<211> 54

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Pro(CCC)5
primer

<400> 165

cggggtacca tgcccccccc cccccccagc aagggcgagg aactgttcac tggc 54

<210> 166

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Pro(CCG)5
primer

<400> 166
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<210> 167
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Pro(CCT)5
primer

<400> 167
cggggtacca tgcctcctcc tcctcctagc aagggcgagg aactgttcac tggc 54

<210> 168
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<223> Description of Artificial Sequence: Pro(CGA)5
primer

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<210> 169
<211> 54
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<220>
<223> Description of Artificial Sequence: Ser(AGC)5
primer

<400> 169
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<210> 170
<211> 54

<220>
<223> Description of Artificial Sequence: Ser(TCG)5
primer

<400> 173
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<210> 174
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<220>
<223> Description of Artificial Sequence: Ser(TCT)5
primer

<400> 174
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<210> 175
<211> 54
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<220>
<223> Description of Artificial Sequence: Thr(ACA)5
primer

<400> 175
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<210> 176
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Thr(ACC)5
primer

<400> 176
cggggtacca tgaccaccac caccaccagc aagggcgagg aactgttcac tggc 54

<210> 177

primer

<400> 180
cggggtacca tgtattatta ttattatagc aagggcgagg aactgttcac tggc 54

<210> 181
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Val(GTA)5
primer

<400> 181
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<210> 182
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Val(GTC)5
primer

<400> 182
cggggtacca tggtcgtcgt cgtcgtcagc aagggcgagg aactgttcac tggc 54

<210> 183
<211> 54
<212> DNA
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<220>
<223> Description of Artificial Sequence: Val(GTG)5
primer

<400> 183
cggggtacca tgggtggtggt ggtggtgagc aagggcgagg aactgttcac tggc 54

<210> 184
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Val(GTT)5
primer

<400> 184
cggggtacca tggttgttgt tgttgtagc aaggcgagg aactgttcac tggc 54

<210> 185
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3'
oligonucleotide common primer

<400> 185
ccggaattct cacttgata ggtggtccat gcc 33